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GenCore version 5.1.6
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Title: Perfect score: Sequence: Database : Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Total number of hits satisfying chosen parameters: Run on: OM nucleic - nucleic search, using sw model Minimum DB seq length: 0
Maximum DB seq length: 200000000 Searched: Scoring table: June 8, 2003, 09:14:16; Search time 6001 Seconds (without alignments)
11634.333 Million cell updates/sec AJ012098
2399
1 ATCTTACATGAACACACAAA.....TGTAAGCACGCACTTCTGAG 2399 2054640 seqs, 14551402878 residues IDENTITY\_NUC Gapext 1.0 GenEmbl: \* gb pat ; gb pi ; gb pr ; gb ro ; gb sts em\_vi:\*
em\_htg\_inv:\*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

NO.	Score	Match	Terrage	5	Ė	
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### ALIGNMENTS

AUTHORS TITLE	REFERENCE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	CRE012098	RESULT 1
Kaminski,A.U. and Happe,T. Isolation and characterization of the hydA gene encoding the Fe-hydrogenase of Chlamydomonas reinhardtii	Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Voivocales; Chlamydomonadaceae; Chlamydomonas.	Chlamydomonas reinhardtii	Chlamydomonas reinhardtii.	Fe-hydrogenase; hydA gene.	AJ012098.1 GI:16945125	AJ012098	Chlamydomonas reinhardtii mRNA for Fe-hydrogenase.	CRE012098 2399 bp mRNA linear PLN 15-NOV-2001		

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2 (bases 1 to 2399)
Happe, T.
Direct Submission
Submitted (15-OCT-1998) Happe T., Molecular Biochemistry,
Institut, Kirschallee 1, D53115-Bonn, GERMANY
Revised by author 31-JAN-2001
Related sequence A/308411.
                                                                                      GCCTAGGCAACGTCGCTTGCGCGGGCTGCCGACCCGCTGCGGAGGCGCCTTTGAGTCATG
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                       Chlamydomonas reinhardtii.
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Eukaryota; Viridiplantae; Chlorophyta;
Chlamydomonadaceae; Chlamydomonas.
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University of Chicago, 1103 E. 57th St., Chicago, IL 60637, USA
Location/Qualifiers
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CTGCCGCACCCGCTGCGGAGGCGCCTTTGAGTCATGTCCAGCAGGCGCCTCGCCGAGCTTG
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llarity 94.2%;
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a 777 c 812 g 449 t
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4 50	D QV	1525 ACGAGAACCCGTCCATCCGCGAGCTGTACGACACGTACCTCGGAGAGCCGCTGGGCCACA 1584
7 C	Ao Ga	- 1585 AGGCGCACGAGCTGCTGCACACCCACTACGTGGCCGGCGGGGGGGG
65 TGACCATCATGGAGGAGGGCAGCGAGCTGCTGCACCGACCACCGACCACCTGGAGGCCC 6	D Qy	1645 AGAAGTGAGGAGCGCCAGAGGCTCTTTGGGCGGAGACAGCTTCAAAGCGAGGGGGCGTAT 1704
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7	dg Qy	1765 GGTCAAAATAGGCGGCGGGTCAAATGTTTCCTTTTTGAGTGGTGTCACAGCATGGGGCAC 1824
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865 GGTTCTGTGTGGACGCCGACCCCTGCGCCAGCTGGACCACGTCATCACCACCGTGG 924	. Qy	1840TAGGCTGTTCACTGCACG 1857  1921 AATGCCTGGTCTCCTTCCACATTGGTGAGCGCGGCTCCGCGTAGGCTGTTCACTGCACG 1980
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985 GGGACAATCCAATGGGCGTGGGCTCGGGCGCGCGCGTGCTGTTCGGCACCACCGGCGGTG 1044	Qy Db	1918 CCTCCAGGGCACGTCGGAATGGCGCGTGCCCATCAACGCAAATTCTTGGCCTTCATCGCT 1977
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1105 TGAGCCTGAGCGAGGTGCGCGGCATGGACGGCATCAAGGAGACCCAACATCACCATGGTGC 1164	Qy Db	2038 TTGGTTGGAAGCTAAACATGTTTGGGAACAATTCATCTTACTAAAGCGTGTGGGGGTTGA 2097
	Ob	098 GGATGC
1225 CCGCCGCGACGGACCCCCGGGCCGCTGGCCTGGGACGGCGGGGCGCGGGCTTCACCAGCG 1284	QV db	2158 GCATACGACAACGGGGCCCGTGAGGATTGAGCACTTGACTCGCGAACTTATGAACGTAGC 2217
1285 AGGACGGCAGGGGGGATCACACTGCGGGTGGCCGTGGCCAACGGGCTAGGGCAACGCCA 1344	Q da	2218 GCTTTATACCCACCGTATGCGAITGACGTTGGTGTAGGCAACCAGGCGGTAGGAAGGCGG 2277
	oy da	2278 AGAGATGCATTGCAAACGCCTGTAAAAGAACGGCATAGCTACTAGACACTCTGATGTGGA 2337
	D OY	2338 CCCTTGGCGCAGCCACGACAGGAGAGGTGTGCATCAGCCGCTTGTAAGCACGCAC
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88.3%; Score 2119.4; DB 8; Length 2454; imilarity 93.7%; Pred. No. 9.2e-253; CCTCANACCCTCGANACCTTTTTCCANCAGTTTACACCCCANTTCGACGCCGCTCCANGC 99 [	/ codon_start=1 /product="iron-hydrogenase HydA" /product="iron-hydrogenase HydA" /protuct="iron-hydrogenase HydA" /protuct="iron-hydrogenase HydA" /protuci="iron-hydrogenase HydA" /protuci="id="AAL23572.1" /db_xref="gi:18026270" /translation="MSALYUKPCAAVSIRGSSCRARQVAPRAPLAASTVRVALATLEA PARRIGVACPAAAPARAEPLSHVQQALAELARCRODDTRKHVCVQVAPAVRVAIAET LGLAPGATTPKQLAEGLRRLGFDEVFDTLFGADLTIMEEGSELLHRLTEHLEAHPHSD EPLPMFTSCCPGWIAMLEKSYPDLIPYUSSCKSPQMALAAMVKSYLAEKKGIAPKOMV MVSIMPCTRKQSEADRDWFCVDADPTLRQLDHVITTVELGNIFKERGINLAETPEGEW DNEMGVGSGGGLLFGTTGGVMEAALRTAYELFTCTPLPRLSLESFYRGMIGIKETMITM VPAPGSKFEELLKHRAAARAEAAAHGTPGPLAWDGGAGFTSEDGRGGITLRVAVANGL GNAKKLITMMQAGBAKYDFVEIMACPAGCVGGGGQPRSTDKAITQKRQAALYNLDEKS TLRRSHENPSIRELYDTYLGEPLGHKAHELLHTHYVAGGVEEKDEKK" 493 a 747 c 784 g 430 t	Dratory, 1617 Cole Boulevard, Golden, CO 80401, USA  Location/Qualifiers  1. 2454  /organism="Chlamydomonas reinhardtii" /strain="21gr" /db xref="taxon:3055" /clone="lam9-1"  1. 2454 /gene="hydA" /gene="hydA" /gene="hydA"	from Chlamydomona rgoing anaerobios nn.D., Seibert, M.	AY055755  AY055755  Complete cds.  AY055755  AY055755  AY055755  AY055755.1 GI:18026269  Chlamydomonas reinhardtii.  Chlamydomonas reinhardtii.  Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.  1 (bases I to 2454)
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Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
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                                   CACCGGCTTGCGTGCGCTTCGACCAGGTGTTTGACACGCTGTTCGCGGCCGACCT
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                                                                                                             CGTTGCCATTGCTGAGTCATTCGGCCTGGCCCCGGGTGCCGTGTCGCCGGGCAAACTAGC
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/ Codon_Start=1
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/ protein_id="AAL23573.1"
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HSDEPLMFTSCCPGWVAMMEKSYPELIFFVSSCKSPOMMGAMVKTYLSEKQGIPAK
DIVMVSUMPCVEKQGEADREWFCVSSERVRDUNDHVITTAELGNIFKERGINLEELPDS
SMDQPLGLGSGAGVLFCTTGGVMEAALRTAYEIVTKEPLPRLNLSEVRGLDGIKEASV
TLVPAPGSKFAELVAERLAHKVESAAVAAVEGAVEPIAYDGGGFSTDDGKGG
LKLRVAVANGLGNAKKLIGKNVSGEAKVEFTENACPAGCVGGGGPRSTDKQITQKR
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                                                                           GTACCTCGGAGAGCCGCTGGGCCACAAGGCGCACGAGCTGCTGCACACCCCACTACGTGGC 1618
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AJ298228.1 GI:18073434
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'Chlorella' fusca.
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Submitted (13-DEC-2000) Happe T.,
Institut der Universitaet Bonn, K
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GCCTCCGCCGCCTCGGCTTTGACGAGGTGTTTGACACGCTGTTTGGCGCCGACCTGACCA
                                                                             CTCCAACACCTCAGGCCAAGCTGCCTCACTGGCAGCAGGCTCTGGATGAGCTCGCCAAGC
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                                                      CTATTGCTGAGACCATTGGCCTTGGCCCCCAGGAGATGTCACCATTGGGCCAGCTCGTGACTG
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LDELAKPKESRELMIAQIASAVRVAIAETIGLAPGDVTIGQAVTGLRMLGFDYVPDTL
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SCKSPQNMLGAVIKNYYAQQVGVQPSDICNVSVMPCVRKQGEADREWFNTTGAGLARD
VDHVYTTAEVGKIFLERGIKLMELPESHFDNPJGEGTGGALFGTTGGVMEAALRTVY
EVVTÖKRMGRVDFEEVRGLEGIKAEBITLKPGDDSPFKAFAGADGQGITLKIAVANGL
GNAKKLIKSLSEGKAKYDFIEWACPGGCTGGGQPRSTDKQTLQKRQQAMYNLDERS
TIRRSHDNPFTQALYDKFLGAPNSHKAHDLLHTHYVAGGIPEEK"
                                                                                                                                                                                                                                                                                                                                                               /gene="hydA"
/product="Fe-hydrogenase"
/EC_number="1.18.99.1"
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/product="Fe-hydrogenase"
/protein_id="CAC83291.1"
/db_xref="GI:18073435"
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/product="Fe-hydrogenase"
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Belaich,J.P.
Characterization of an operon encoding
in Desulfovibrio fructosovorans
J. Bacteriol. 177 (10), 2628-2636 (1995)
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vakffldftmbetckgyfpcrigskalyfildritkgkgtrabldrlksiesiiktor
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VAMEAMQDEVAKNGLTGVEFMQSSCMTYCYAEPTVEITLPGKDPVVFGGVDENRAREL
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CFVKGADKVVHAFKEQLKIDIGDVTPDGRFSIDTLRCVGGCALAPIVMVGEKVYGNVT
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                                            cTGCGCACGGCCTATGAGCTGTTCACGGGCACGCCGCTGCCGCGCCTGAGCCTGAGCGAG
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ACPGGCIGGGGQYHHGDVELLKKRTQVLYAEDAGKPLRKSHENPYIIELYEKFLGKP
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Florin,L., Tsokoglou,A. and Happe,T.

Florin,L.) Trookoglou,A. and Happe,T.

A Novel Type of Iron Hydrogenase in the Green Alga Scenedesm obliquus Is Linked to the Photosynthetic Electron Transport J. Biol. Chem. 276 (9), 6125-6132 (2001)
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AJ271546
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/translation="MPEMOPGGRYAVGVRPPVRVAIAETMGLNPGDVTVGOMVT
GLRMLGFDYVFDTLFGADLTIMEEGTELRHRLODHLEGHPNKEEPLPMFTSCCPGWVA
MVEKSNPELIPYLSSCKSPOMMLGAVIKNYFAAEAGAKPEDICNVSVMPCVRKOGEAD
REMFNTTGAGGANVDHYMTTAELGRIFFERGIKLNDLOBSPFDNPVGEGSGGGVLFGT
TGGVMEAALRTVYEVTOKPLDRIVETSVFGLEGIKESTLHLTBGFSPFRFAGABG
TGITLNIAVANGLGNAKKLIKOLAAGESKYDFIEVMACPGGCIGGGOPRSADKOILO
KROAMYDLDERAVIRRSHENPLIGALYEKFLGEPNGHKAHELLHTHYVAGGVPDEK"
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/gene="hydA"
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2622. .3089,3401. .3877)
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/gene="hydA"
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1289. .1663
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db_xref="taxon:3088"
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                                             DFHYDABG

D. fructosovorans hydA and hydB ger

Y11759

Y11759.1 GI:1914863

Fe-hydrogenase; hydB gene; hydB ge
Desulfovibrio fructosovorane.

Desulfovibrio fructosovorane
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1 (bases 1 to 2887)
Casalot, L., Hatchikian, E.C.,
                         Desulfovibrio.
                                   Bacteria; Proteobacteria;
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/gene="hydA"
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/gene="hydA"
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/gene="hydA"
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'gene="hydA"
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Pred. No. 2.1e-21;
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 Forget, N.,
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                                  488
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Joseph Aiguier, Marseille, 13402 Cedex 09, FRANCE
Location/Qualifiers
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2 (bases 1
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Molecular study and partial purification on iron-only hydrogenase in Desulfovibrio fructosovorans
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Direct Submission
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                                                                                                                                                                                    GGCGCTCGCCGAGCTTGCCAAGCCCCAAGGACGACCCCACGCGCAAGCACGTCTGCGTGCA
                     CACCCCAAGCAGCTGGCCGAGGGCCTCCGCCTCGGCTTTGACGAGGTGTTTGACAC
                                                                                                    GGTGGCTCCGGCCGTTCGTGTCGCTATTGCCGAGACCCTGGGCCCTGGCGCCCGCGGCCGCCAC
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                                                                                                                                                                                                                                                                                                                    613
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/protein_id="CAA72423.1"
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/db_xref="SPTREMBL:008311"
                                                                                                                                                                                                                                                                                                                1824. .1925
/gene="hydB"
a 985 c
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/product="cytochrome-c3 hy
/protein_id="CAA72424.1"
/db_xref="G1:1914865"
/db_xref="G1:1914865"
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/gene="hydB"
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456. 1721
/gene="hydA"
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/EC number="1.12.2.1"
/function="Fe-hydrogenase large
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/translation="MSILATTRRGFMKTACVLTGGALIGLRLTSKAVAAAKQLKEYMM
DRVNAVYGADAKFKVRASQDNAQVITLYKKFLHEPLSHESEHLLHTKWVDRSKDLAAL
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LARITKKLDKPLPQTTSCCEGWQKYAETFYPELLPHFSSCKSPIGMMGPLAKTYCAPK
LGYEPKQIYTVSIMCTTAKKFEGKMREMDASGFRDIDATINTRELAYVMKKAGIDLPK
IANGKRDAVMGESTGGATIFGVSGGVMEAALRFAYQALTKKPPQSWDFKAVRGLNGIK
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CPTGAITGESGEPHKVVDPAACINCGQCLTHCPVAAIYETVSFVPEIEAKLKDKNVKV
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strain="DSM 3604"
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D.vulgaris oxamicus (strain Monticello)
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                        /translation="MSRIEMEKIFYEDHAPDPKADPDKLFF101DESKCIGCDSCOQY
CPTGALFGDTGDAHKIPHEELCINCGQCLTHCPVGAIYESQSWVTBIEKKIKAKDVKV
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VORLTKKLDKELPQTTSCCIGGWHKYVESLYBELFPHMSSCKSPIGMLGTLAKTYGADR
MKYDRAKVYTVSIMPCTAKKYEGMRPOLWDSGHKDIDATIDTRELAYMIKKAKIDFADK
MKYDRAKVYTVSIMPCTAKKYEGMRPOLWDSGHKDIDATIDTRELAYMIKKAKIDFA
                                                                                                                                                                                                                                                  GVLEAADRRSTRMYAGLKKRLAMASASRA"
                                                                                                                                                                                                            1514. .1888
/note="[Fe]-hydrogenase beta subunit"
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/transl_table=11
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/db_xxef="GI:145099"
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/db_xref="taxon:881"
237. .1502
                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="[Fe]-hydrogenase
                 Score 222; DB 1;
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Nucleotide sequence of the gene encoding
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/strain="(Hildenborough)"
/db xref="taxon:B81"
  /note="inverted
                                        note="inverted
                                                                                      note="put. transcription terminator"
                                                                                                                                      'note=" (weak)
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                                      | GCTGACCGCGACTGGTTCTGTGGACGCCGACCCCACCCTGCGCCAGCTGGACCACGTC
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CPTAALIGEMGEPHS IPHIEACINCGCCLTHCENAITEAGCSWYEVEKKLKDGKVKC
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EATUNVGGTDVKVAVVHGAKRFKQVCDDVKAGKSPYHFIEVMACPGGCVCGGGQPVMP
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/db_xref="SWISS-PROT:P07603"
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DRINGYYGADAKFPVEASQDNTQVKALYKSYLEKPLGHKSHDLLHTHWFDKSKGVKEL
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/transl_table=11
/protein_id="CAA26266.1"
/db_xref="GI:40830"
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/note="13.5-kDa protein (aa 1-123)"
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                       'gene="hydA"
/EC_number="1.18.99.1"
/function="hydrogen metabolism"
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                                                                                                                                                                                      TCAAGAGCCTGTCAGAGGGCAAGGCCAAGTATGATTTCATTGAGGTCATGGCATGCCCTG
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1773. .>2246
/gene="hydA"
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a 803 c
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FGADLTIMESCTELLHRLQDHLBCDHPMKEEPLDMFTSCCPGWANVEKSNPELIFPLS
SCKSPQMMLGAVIKWYXAQQVGVOPSDICNUSVMPCVAKQGAADREWFRTTGAGLARD
VDHVVTTAEVGKIFLERGIKLNELPESNFDNPIGEGTGGALLFGTTGGVMEAALRTVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="Fe-hydrogenase"
/EC number="1.18.99.1"
<67. .363</pre>
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GNAKKLIKSLSEGKAKYDFIEVMACPGGCIGGGGQPRSTDKQILQKRQQAMYNLDERS
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/gene="hydA"
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71.1%;
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Pred. No. 4e-14;
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Submitted (15-JAN-1999) Departement de Biologie Moleculaire et
Structurale, CEA-Grenoble, 17 rue des Martyrs, Grenoble 38054,
France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2585 bp DNA linear BCT 25-APR-201
Megasphaera elsdenii putative ABC transporter (abc) gene, partial
cds; and Fe-only hydrogenase (hydA) gene, complete cds.
AF120457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Megasphaera elsdenii.
Megasphaera elsdenii
Bacteria; Firmicutes; Clostridia; Clostridiales;
Acidaminococcaceae; Megasphaera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 2585)
Atta, M. and Meyer, J.
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Characterization of the gene encoding the [Fe]-hydrogenase from
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                                663
                                                                               /Codon_start=1
//trans[_table=11
//trans[_table=11
//trans[_table=11
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//db xref="GI:665985"
//db xref="GI:665985"
//db xref="GI:6659865"
//db xref="GI:66598665"
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/strain="ATCC25940"
/db_xref="ATCC:25940"
/db_xref="taxon:907"
                  2502. .
740
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YQQEIGHTVTNQFGQRLSATRLLDQFLFTEEMQYTY1AKLSGGERRLYLLRLLMDQF
NVLLLDEFTNDLDIFTLTVLRRYLDTFQGVLVLVSHDRYFLDRVDKLFTLEKGTDDF
FYGDYSEYLEEKYSHHQEKKGEKATAPSITKTNITPAKTKAGLTSRQEEELRRITEEL
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998. .1002
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/transI_table=11
/product="putative ABC transporter"
/protein_id="AAF22113.1"
/db_xref="GI:6650984"
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1012. .2466
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TITLE	ORGANISM REFERENCE AUTHORS	RESULT 14 AE001705 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE	Qy 1 Db 1	Db 1	Qу 1	Qy 1	Qy Db 1	Qy Db 1	Qy Db	Оу Дъ 1	Qу рь 1	Qy Db	Qу 1	Оу Db 1:	Query Match Best Local Matches 39
r.R., Malek,J.A., Linher,K.D., Garret ), Pratt,M.S., Phillips,C.A., 19,J., Sutton,G.G., Fleischmann,R.D., et al. et al. et ransfer between Archaea and bacte Thermotoga maritima	ricina rmotogae; Thermotogae; Thermotogales; Thermotogacea o 15158) clayton,R.A., Gill,S.R., Gwinn,M.L., Dodson,R.J., Clayton,R.A., Beterson,J.D., Nelson,W.C., Ketchum,K.A.	rit 1:4	059 CTGCGCACGGCCTATGAGCTGTTCACGGGCACGCCGCTGCCG 1100	999 GSCGINGGSCINGGGGGCGGTGCTGTTUGGCACCACCGGGGGTGTCATGANGGCGGGG 1058	39 TTCAAGGAGCGCGGCATCAACCTGGCCGAGCTGCCCGAGGGCGACGACTGGGACAATCCAATG 998	879 GCCGACCCCACCCTGCGCCAGCTGGACCACGTCACCACCGTGGAGCTGGGCAACATC 938	831 TGCACGCGCAAGCAGTCGGAGGCTGACCGCGACTGGTTCTGTGTGGAC 878	771 TACCTAGCGGAAAAGAAGGCATCGCCCCAAAGGACATGGTCATGGTGTCCCATCATGCCC 830	711 ATCCCCTACGTGAGCAGCTGCAAGAGCCCCCAGATGATGCTGGCGGCCATGGTCAAGTCC 770	651 ATGITCACCAGCTGCTGCCCCGGCTGGATCGCTATGCTGGAGAAATCTTACCCGGACCTG 710	591 CTGCTGCACCGCCTCACCGAGCACCTGGAGGCCCACCCGCACTCCGACGAGCCGCTGCCC 650	531 GACGAGGTGTTTGACACGCTGTTTGGCGCCGACCTGACCATCATGGAGGAGGGCAGCGAG 590	471 CTGGCGCGGGCGCCACCACCCCAAGCAGCTGGCCGAGGGCCTCCGCCTCGGCTTT 530	411 AAGCACGTCTGCGTGCAGGTGGCTCCGGCCGTTCGTGTCGCTATTGCCGAAGACCCTGGGC 470	tch 7.5%; Score 180.8; DB 1; Length 2585; al Similarity 56.6%; Pred. No. 1.9e-13; 397; Conservative 0; Mismatches 272; Indels 33; Gaps 2;

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JOURNAL
MEDLINE
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2 (bases 1 to 15158)
2 (bases 1 to 15158)
Nelson, K.E., Clayton, R.A., Gill, S.R., Gwinn, M.L., Dodson, K.U., Haft, D.H., Hickey, E.K., Peterson, J.D., Nelson, W.C., Ketchum, K.A., McDonald, L., Utterback, T.R., Malek, J.A., Linher, K.D., Garrett, M.M., Stewart, A.M., Cotton, M.D., Pratt, M.S., Phillips, C.A., Richardson, D., Heidelberg, J., Sutton, G.G., Fleischmann, R.D., Milliand, C.S., Salzberg, S.L., Smith, H.O., Venter, J.C. and Fraser, C.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 399 (6734), 323-329 (1999) 99287316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0360571
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139. .2601
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y; putative"
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Query Match
Best Local Similarity
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/product="ATP-dependent DNA helicase"
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Submitted (15-JAN-1991) J.P.W.G. Stokkermans,
Wageningen, Dept of Biochemistry, Dreijenlaan
Wageningen, The Netherlands
2 (bases 1 to 1940)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hyd Gamma, a gene from Desulfovibrio vulgaris (Hidenborough) encodes a polypeptide homologous to the periplasmic hydrogene FEMS Microbiol Lett. 58, 217-222 (1989)
Data kindly reviewed (14-MAR-1991) by Stokkermans J.
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                               /Godon_start=1
/transI_table=11
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/product="Hyd_gamma"
/protein_id="CAA40970.1"
/db_xref="GI:40828"
/db_xref="GI:40828"
/db_xref="SpTREMBL:0946606"
/db_xref="SpTREMBL:0946606"
/translation="MNAFINGKEVRCEPGRTILEAARENGHFIDTLCELADIGHAPGT
/translation="MNAFINGKTVPEEGMRITTIEAARENGHFIDTLCELADIGHAPGT
CRVCLVEIMRDKEAGPGIVTSCTTPVEEGMRITTIEAARENGHFIDTLCELADHDHDC
AACARHGDCELODVAAQFVGLTGTRHHFPDYAASRTRDVSSPSVVEMMGKCITCLRCVA
VCRNVQGVDALVYTGNGIGTEIGLRHNRSQSASDCVGCGQCTLVCPVGALAGRDDVER
VLDYLYDPEIVTVFQFAPAVRYGLGEEEGLPPOSSVEGCYPTALRILGADVVLDTWFA
ADLVIMEEGTFELORJRGGAKLELPTTSCCFGGWVNFAEKHLPDILPHVSTTRSPOCCLG
ALAKTYLARTMNVAPERMRVVSLMPCTAKKEEAARPEFRRDGVBDVDAVLTTREFARL
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/strain="Hildenborough"
/db_xref="taxon:881"
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                           CGCGCGCGCGAGGCCGCCGCG 1232
                                                                                                                                                        GCCGCTGCCGCGCGTGAGCCTGAGCGAAGGTGCGCGCATGGACGGCATCAAGGAGACCAA 1150
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TGCCCGGCAGATGGTCGAGGCG 1518
                                                             CGTCCCGCTTGGTGAGGGTAACGGTTCCGTGAAGGTCGCCGTGGTGCATGGGCTCAAGGC
                                                                                          CATCACCATGGTGCCGGGGCCCGGGGTCCAAGTTTGAGGAGCTGCTGAAGCACCGCGCCGC 1210
                                                                                                                      TACGACAGGCGGGTAATGGAGGCGGCACTGCGTACGGTCTACCATGTGCTGAACGGCAA 1376
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NLSHRLLHTRYGDRKSEVAYTMRDIWHEMTLGRRVRGDSD"
1892. .1918
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Search completed: June 8, 2003, 11:53:21 Job time: 6045 secs

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Title:
Perfect score:
Sequence:
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Maximum DB seq length: 200000000
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75
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
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10270.996 Million cell updates/sec
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Match Length DB
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Copyright (c) 1993 - 2003 Compugen Ltd.
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3.9 1737
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3.0 1572
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AAD17184
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                                                             Micromonospora DNA
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Human NADP hydroge
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Human adenosine Al
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Nucleotide sequenc	AAV11297	19	1248	2.6	63.4	45
lavuligeru	AAD14507	22	18	•	63.4	44
Synthetic Pol poly	ABL39983	24	3015	•		43
fied HIV-1	AAA51951	21	54	٠		42
ied HIV-	195	21	2322	٠	·	
e herpes		12	3993	٠	'n	
gene.	AAQ14478	12	46	٠		
Streptococcus olea	AAA09469	21	93	٠		
Platenolide syntha	AAT80414	18	4		<u>ب</u>	
enolide s	85	18	44377	•	5	
c Env	ABL39955	24	2550		7.	
HIV gp160 with sig	AAA51615	21	2547	2.8		34
0 000	AAA51614	21	2466		7.	
Human polynucleoti	AAC91328	22	2113		7.	
doreduct	AAH24245	22	2101		7.	
HIV gp140 coding r	AAA51613	21	1944	٠	7.	
	AAV21187	19	53789		8	
Synthetic Pol poly	ABL40024	24	3009	2.9	æ	
	AAD17185	22	27541	٠	9	
conic	AAA70471	21	4689		9	
bicistronic c	AAA70473	21	4608	٠	9.	
gp160.mods	AAA70445	21	2547		φ.	
gp160.modSF	044	21	2466	٠	9	
ified HIV-1	AAA51966	21	2358		69.8	22
gp160.modSF	AAA70447	21	2358	•	9	
fied HIV-1	AAA51948	21	2334		9	20
fied HIV-1	AAA51947	21	2328	•	9	
fied HIV-1	AAA51946	21	2322	•	9	18
<pre>fied HIV-1</pre>	194	21	2316	•	69.8	17
ied HIV-1	AAA51945	21	2316	•	9	16
Modified HIV-1 Env	194	21	31		9	15
V gp140		21	2025		9	14
V gp140.mod	AAA70433	21	2	2.9	9	13
V gp140.mut	043	21	94	•	φ.	12
V gp140.	704	21	1944	2.9		11
HIV gp140.modSF162	AAA70434	21	1944	2.9	٠	10

### ALIGNMENTS

PS XX	PT	ΡŢ	×	뮸	×	PA	PΑ	×	PR	X	PF	X	đđ	X	Nd	×	20	ž	즟	Š	×	DH	×	ဌ	×	AC	×	ĬD	RESULT 1
Example 4; Fig 10; 12pp; Japanese.	for production of hydrogen and is environmentally friendly	Preparation of heterologous hydrogenase in blue-green algae - useful		WPI; 1999-583699/50.		(CHIK-) ZH CHIKYU KANKYO SANGYO GIJITSU KENKYU.	(AGEN ) AGENCY OF IND SCI & TECHNOLOGY.		13-MAR-1998; 98JP-0062601.		13-MAR-1998; 98JP-0062601.		21-SEP-1999.		JP11253166-A.		Clostridium pasteurianum.		Shine-Dalgarno; ss.	Clostridium; hydrogenase; blue-green alga; hydrogen; microbe;		Clostridium pasteurianum hydrogenase #2.		13-DEC-1999 (first entry)		AAZ25199;		AAZ25199 standard; DNA; 1737 BP	LT 1 5199

AAA70438

Streptomyces nours Streptomyces nours HIV gp140.mut.modS

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A method has been developed for the preparation of hydrogenase in which CC a blue-green alga introduced by a recombinant vector containing a CC heterologous hydrogenase gene is cultured in a medium to form and CC heterologous hydrogenase in the microbe body. Also claimed are: (1) a CC blue-green alga introduced by a recombinant vector containing a gene CC having a Shine-Dalgarno sequence consisting of AAGGAA upstream of the hydrogenase structural gene derived from a Clostridium genus microbe; (2) a method for the production of hydrogen by culturing the above CC blue-green alga under light irradiation; (3) a method for the production of hydrogen by culturing the above blue-green alga anaerobically and conflydrogen by culturing the above blue-green alga anaerobically conflored by reacting the above blue-green alga with an electron CC hydrogen by reacting the above blue-green alga with an electron CC then under light irradiation; (4) a method for the production of the production of CC then under light irradiation; (4) a method for the production of the production of CC then under light irradiation; (4) a method for the production of the production of CC then under light irradiation; (5) a method for the production of the production of CC then under light irradiation; (6) a method for the production of hydrogen by culturing the above blue-green alga anaerobically and then reacting it with an CC electron receptor. The method is mild to environment. The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               represents a Clostridium pasteurianum hydrogenase nucleotide from an example from the present invention.
                                                                          GCTGCGCACGGCCTATGAGCTGTTCACGGGCACGCCGCTGCCGCCTGAGCCTGAGCCGA
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TCTGCGGAGTGCAAAAGACTTTGCTGAAAACGCTGAACTTGAAGATATCGAATATAAGCA
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Pred. No. 1.1e-07;
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Query Match Best Local Similarity

3.5**%**; 31.5**%**;

Score Pred.

83.2; DB 20; No. 7.6e-06;

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                                                                                        The specification describes antisense oligonuclectides (AAX52869-X55271) CC directed against at least 2 mRNAs selected from target genes, coding and con-coding regions of RNAs corresponding to target genes, gene coding and the juxta-section between coding and non-coding regions, intron-exon borders, the complete the coding and the juxta-section between coding and non-coding cregions and all segments of RNAs encoding proteins associated with one coding and another coding cregions and all segments of RNAs encoding proteins associated with one coding conditions are those associated with impaired respiration and conditions are those associated with impaired respiration and conditions are those associated with impaired respiration, impeded conditions are those associated with impaired respiration and confinemation, allergic rhinitis, acute asthma, allergies, asthma, impeded crespiration, respiratory distress syndrome, pain, cystic fibrosis, complete the pulmonary disease (COD) and cancers such as leukemias, code constructive pulmonary disease (COD) and cancers, lung cancer, melanoma, part astaccare, swell as all types of cancers which may metastasize to the partic metastases, as well as all types of cancers which may metastasize to the conditions of the cancer which may metastasize to the conditions of the cancer which may metastasize to the conditions of the cancer which may metastasize the conditions o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antisense oligonucleotide; multiple target; antisense treatment; impaired respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation; allergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary distress syndrome; pain; cystic fibrosis; pulmonary hypertension; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer; hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX53491 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 37; 120pp; English
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   CCCGACGCCGANHNNNSGCCCGGCCCGACGCCGAVNHNNNSGCCCGGCCCGACG 103972
                                                         ACGTCATCACCACCGTGGAGCTGGGCAACATCTTCAAGGAGCGCGGCATCAACCTGGCCG
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The specification describes antisense oligonucleotides (AAX52869-X55271) directed against at least 2 mRNAs selected from target genes, coding and conn-coding regions of RNAs corresponding to target genes, gene coding and controlled the selected from target genes, gene coding and controlled the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one cor more diseases, conditions or mixtures. The antisense oligonucleotides conditions or mixtures. These multiple target conjectures (specifically AAX55180-771) can be used for the conjecture those associated with impaired respiration and conditions are those associated with impaired respiration and conditions are those associated with impaired respiration and confilammation, including lung diseases, pulmonary vasoconstriction, impeded crespiration, respiratory distress syndrome, pain, cystic fibrosis, cut obstructive pulmonary disease (COPD), and cancers such as leukemias,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               impaired respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation; allergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary distress syndrome; pain; cystic fibrosis; pulmonary hypertension; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; brast cancer; lung cancer; pancreatic cancer; hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
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                                                   CACCACCGTGGAGCTGGGCAACATCTTCAAGGAGCGCGGCATCAACCTGGCCGAGCTGCC
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                                                                                                                                                                                                                                                                                                                    CGGGCCGSNNNDNNBGGCCBGGGCGCCGCCGGCCGGGC-CGSNNNDNNGGCCBGGGCG
                                                                                                                                                                                                                                                                                                                                                   CGCGCCAAAGGACATGGTCATGGTCCATCATGCCCTGCACGCGCAAGCAGTCGGAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNNNDNNCCGCBGGCCSNNNDNNCGCBGGCCBGGGCGCCGCCGGCCGGCCGGSNNNDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGGATCGCTATGCTGGAGAAATCTTACCCGGACCTGATCCCCTACGTGAGCAGCTGCAA
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                                                                                                                    CGAGGGCGAGTGGGACAATCCAATGGGCGTGGGCTCGGGCGCGCGGCGTGCTGTTCGGCAC
                                                                                                                                                                                    GGGCGCGCCGGCCGGGCCGSNNNDNNCBGGGCGCGCCGCCGGCCGGCCGSNNNDNN
                                                                                                                                                                                                                                                                                  TGACCGCGACTGGTTCTGTGTGGACGCCGACCCCACCCTGCGCCAGCTGGACCACGTCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6071 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29417 C; 36712 G; 21328 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 72.6;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ore 72.6; DB 20;
ed. No. 0.00058;
Mismatches 742;
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RESULT 5.
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                          Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                      Ota T,
Ishii
                                                                                                                                                                                                                                                                                                                                                            Human
                                                                                                                                                                                                                                                              28-JUL-2000;
                                                                                                                                                                                                                                                                                                  EP1074617-A2
                                                                                                                                                                                                                                                                                                                                        Human;
                                                                                                                                                                                                                                                                                                                                                                               26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                AAH13714;
                                                                                                                                    WPI; 2001-318749/34.
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                                                                                  full-length
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                                                                 8; SEQ ID
                                                                                                                                                                                                                                                                                                                                                            CDNA
                                                                                                                                                                                                                                                                                                                                        primer;
                                                                                                                                                     Isogai T,
, Sugiyama
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                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
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                                                                                                                                                                                                                                                                                                                                                            sequence
                                                                                                                                                                                                    99JP-0248036.

99JP-0300253.

2000JP-0118776.

2000JP-0183767.

2000JP-0241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105654
                                                                                                                                                                                                                                                                                                                                         detection;
                                                                 10601;
                                                                                                                                                     Nishikawa T,
T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA;
                                                                                                                                                                                                                                                                                                                                                           SEQ ID
                                                                2537pp
                                                                                                                                                                                                                                                                                                                                         diagnosis;
                                                                                                                                                                                                                                                                                                                                                            NO:10601
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                                                                 G
                                                                                                                                                     Hayashi
A, Naga
                                                                  ROM;
                                                                                                                                                      ashi K,
Nagai F
                                                                                                                                                                                                                                                                                                                                         antisense therapy;
                                                                 English
                                                                                                                                                       <u>,</u>7
                                                                                                                                                      Saito K,
Otsuki
                                                                                                                                                                 Yamamoto
                                                                                                                                                                                                                                                                                                                                         gene
                                                                                              detection by the
                                                                                                                                                                                                                                                                                                                                          therapy;
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination

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RRSULT 6
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ID AA442
XX AA427
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Best Local Similarity
Matches 159; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide which comprises at least 15 nucleotides and the combination of oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the 5'-end sequence]3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAH3633 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the name of the process.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human
   27-OCT-2000; 2000WO-CN00377
                                                                  03-MAY-2001
                                                                                                                                                                                                                                                                                                                                        Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                 NADP hydrogenase subunit 50; cancer; haemopathy; HIV infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH27127
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                                                                                                                               WO200130824-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NADP hydrogenase subunit 50 cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCGGCGGCCAGCCCCGCTCCACCGACAAGGCCATCACGCAGAAGCGGCAGGCGGCGCTGT 1488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                 disease; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1419
                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                        product=
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52.1%;
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                                                                                                                                                                                        "NADP hydrogenase subunit
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .00075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146;
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RESULT 7
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to NADP hydrogenase subunit 50. Included in the invention are nucleotide and amino acid sequences for NADP hydrogenase 50 subunit, a vector containing the cDNA sequence, a host cell transformed with the vector, and an antibody directed against the protein. The polypeptide and polynucleotide can be used in the diagnosis and treatment of cancer, haemopathy, HIV infection, immunological diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NADP hydrogenase subunit 50 and encoded polynucleotide, applicable in diagnosis and treatment of cancer, hemopathy, HIV infection, immunological diseases and inflammation -
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 CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hydrogenase subunit 50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6; Page 25-26; 33pp; Chinese.
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P-PSDB; AAB97260.
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                                            Streptomyces
                                                                       Polyketide antifungal;
                                                                                                                  Streptomyces noursei nysl DNA of nystatin PKS
                                                                                                                                               29-NOV-2001
                                                                                                                                                                            AAD17184;
                                                                                                                                                                                                      AAD17184 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCGGCGAGGCCAAGTACGACTTTGTGGAGATCATGGCCTGCCCCGCGGGGCTGTGTGGGCCG
                                                                                                                                                                                                                                                                                 CGTAC
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                                                                       synthase; PK antibiotic;
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                                            noursei
                                                                                                                                               (first entry)
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Location/Qualifiers complement (1..1035)
                                                                                                                                                                                                        DNA; 65140
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                                                                          PKS; macrolide; nystatin; ic; nys1; ds.
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                                                                         nys1;
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                                                                                                                  gene cluster.
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10-APR-2000;
14-APR-2000;
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                               WPI; 2001-557614/62.
P-PSDB; AAE10125, AAE10126, AAE10127, AAE10128, AAE10129, AAE10130, AAE10131, AAE10132, AAE10133, AAE10134, AAE10135, AAE10136, AAE1013
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(BRAU/)
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(ALPH-)
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                                                                                                                                                                                                                                   (DZIE/)
nystatin polyketide synthase polynucleotides and polypeptides.
                                                                                  / SB, Senc.
S, Ellingsen 7
                                                                                                                                             DZIEGLEWSKA H.

ZOTCHEV S B.

ZOTCHEV S B.

SEKUROVA O N.

PJAERVIK E.

BRAUTASET T.

STROM A R.
                                                                                                                                                                                                                                                                                   UNIV NORGES TEKNISK NATURVITENSKAPELIGE SINTEF STIFTELSEN IND TEK FORSK.
                                                                                                                                                                                                                                               ALPHARMA AS.
SINVENT AS.
                                                                                                                                                                                                                                                                                                                                ; 2000GB-0002840.
; 2000GB-0008786.
; 2000GB-0009387.
                                                                                              Sekurova ON,
lingsen TE,
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/note= "CDS does not include stop
complement (1056..2576)
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/note= "CDS does not include
complement (62551..63615)
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Sletta H, Gulliksen O;
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   1057 CGCTGCGCACGGCCTATGAGCTGTTCACGGGCACGCCGCTGCCGCGCCTGAGCCTGAGCG 1116
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                                  CGGGACTGGGCGCCGACCACCGCTGCTCGGCGCCACCGTCGAACTCGCCGACGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGGCAGCGAGCTGCACCGCCTCACCGAGCACCTGGAGGCCCCACCCGCACTCCGACG
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The present invention relates to the cloning and sequencing of the cluster encoding a modular type I polyketide synthase (PKS) enzyme involved in the biosynthesis of the macrolide antibiotic nystatin
The nystatin PKS is useful as antifungal antibiotics. The present sequence is a Streptomyces noursei nysl DNA of nystatin PKS gene
                                                                                                                                                                                                                                                                                                                             antibiotics and
                                                                                                                                                                                                                                               116-151;
                                                                                                                                                                                                                                           266pp; English.
                                                                                                                                                                                                                                                                                                                         antifungals
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Conservative 2.9%; 42.5%; 8270 A; 25171 C; Score 70.2; DE Pred. No. 0.001 0; Mismatches 0 22273 G; 9426 .0015; DB 22; 758; Length 65140; T; Indels other; 18; Gaps cluster. gene w

AGGCGCCGCACGCCTAGGCAACGTCGCTTGCGCGGCTGCCGCACCCCGCTGCGGAGG GCTTTGACGAGGTGTTTG-----ACACGCTGTTTGGCGCCGACCTGACCATCATGGAGG GGCCCACCTCCGTCGTCGCCGGCCACCGAGGAAGCCGTCGCCGCGATCGGGGCGCGCT TCATGGACCCGATGCTGGCGGAATTCCGCGCGCCGTCGCCGGGCCTGACCTACCACGAGC TCACCGCCCAGGACCGCAAGACCACCCGGCTGCGGGTCAGCCACGCCTTCCACTCGCCGC cececaaecacereceaecacececececerecececerarreceaeaecec CCACCGAGGACGÁGGTCACCCCCCACCTCACCGÁCGACGTCTCGATCGCCGCCGTCAACG CGCCTTTGAGTCATGTCCAGCAGGCGCTCGCCGAGCTTGCCAAGCCCAAGGACGACCCCA AGCTCGCCGCGCGCACGTCGCCGGGGGTCCTCTCCCTCGAAGACGCCTGCACCCTCGTCG 18755 525 465 405 18515 18815 579 18695 18635 18575 345 285

CCGCCGACTACTGGGTCCGCCACGTCCGCGAGGCGGTCCGCTTCGCCGACGGCGTCACCG AGCCGCTGCCCATGTTCACCAGCTGCTGC---CCCCGCTGGATCGCTATGCTGGAGAAAT CGCGCATCCCGGTCCTCTCCAACCTCACCGGCACCGTCGCCGCCGTCGCCGACCTGTGCT 696 18935

639

CCCTCACCGACCGCGGCGTGACCACGCTCGTCGAACTCGGCCCGGACGGCGTGCTGTCCG CTTACCCGGACCTGATCCCCTACGTGAGCAGCTGCAAGAGCCCCCAGATGATGCTGGCGG

CCATGGTCAAGTCCTACCTAGCGGAAAAGAAGGGCATCGCGCCAAAGGACATGGTCATGG

TGTCCATCATGCCCTGCACGCGAAGCAGTCGGAGGCTGACCGCGACTGGTTCTGTGTGG CCATGGCCCAGGAATCCCTGCCGGACGGCGCCGCCGCCGTGCCGCTGCTGCGCAAGGACC 1905

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RESULT 8
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/note= "CDS does not include
complement (59045..60241)
                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
6337..34771
   complement
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                    note= "CDS
                                   product= "NysN protein"
                                                                                                                                   product= "NysL protein" complement (58786..58980)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Valla
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(SNTF)
(ALPH-)
(SINV-)
(DZIE/)
(ZOTC/)
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10-APR-2000;
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P-PSDB; AAE10143, AJ
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DZIEGLEWSKA H.
DZIEGLEWSKA H.
ZCTCHEV S B.
SEKUROVA O N.
FJAERVIK E.
BRAUTASET T.
STROM A R.
                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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/product= "NysD2
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TELSEN IND TEK FORSK.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
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Barnett S,
Greer C, S
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01-DEC-1999;
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Greer C,
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Claim 19; Fig
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                                                                                                    24; 391pp; English
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The present invention relates to synthetic HIV protein expression cassettes. The present sequence is the coding sequence of a synthetic HIV Env expression cassette. In, addition, synthetic HIV Gag expression cassettes have been constructed. The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post-entry steps in viral replication. The expression cassettes of the present invention may be used for the recombinant expression of HIV Gag-polypeptides which may then be used to vaccinate against HIV infection and acquired mmunodeficiency syndrome (AIDS).

Sequence 1944 BP; 450 A; 656 C; 577 ဌ 261 T; 0 other;

Query Match Best Local S Matches 422

Similarity

2.9%;

Score 69.8; Pred. No. 0. Mismatches

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                     The present invention relates to synthetic HIV protein expression cassettes. The present sequence is the coding sequence of a synthetic HIV Env expression cassette. In, addition, synthetic HIV Gag expression cassettes have been constructed. The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, viric maturation after particle release and early post-entry steps in viral replication. The expression cassettes of the present invention may be used for the recombinant expression of HIV Gag-polypeptides which may then be used to vaccinate against HIV infection and acquired immunodeficiency syndrome (AIDS).
                                                                                                                                                                                                                    Expression cassettes encoding the human immunodeficiency virus Gag-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficiency syndrome (AIDS) -
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01-DEC-1999;
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Query Match 2.9%; Best Local Similarity 44.3%; Matches 422; Conservative

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Score 69.8; Pred. No. 0. Mismatches

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Greer C, Selby
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ATCATGCCCTGCACGCGAAGCAGTCGGAAGGCTGACCGCGACTGGTTCTGTGTGGACGCC
                             CTGCAGGCCCAGTTCGGCAACAAGACCATCGTGTTCAAGCAGAGCAGCGGCGGCGACCCC
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Expression cassettes encoding the Gag-containing polypeptide useful

human immunodeficiency virus for vaccinating against HIV

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                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGCCCTGCCGCATCAAGCAGATCATCAACCGCTGGCAGGAGGTGGGCCAAGGCCATGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGGAGCGCGCATCAACCTGGCCGAGCTGCCCGAGGGCGAGTGGGACAATCCAATGGGC
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GGCGTGGCCCCCACCAAGGCCAAGCGCCGCGTGGTGCAGCGCGAGAAGCGCGCCGTGACC 1512
                                                                                                         ATGCGCGACAACTGGCGCAGCGAGCTGTACAAGTACAAGGTGGTGAAGATCGAGCCCCTG
                                                                                                                                                      GTGCGCGGCATGAACGAGAGACCAACATCACCATGGT----GCCCGCGCCCCGGG
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                                               TCCAAGITTGAGGAGCTGCTGAAGCACCGCGCGCGCGCGCGCGCGAGGCCGCCGCCGCAC 1235
                                                                                                                                                                                                              CGCGACGGCGGCAAGGAGATCAGCAACACCACCGAGATCTTCCGCCCCGGCGGCGGCGAC 1392
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Pred. No. 0
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                                                                                        The present invention relates to synthetic HIV protein expression cassettes. The present sequence is the coding sequence of a synthetic HIV Env expression cassette. In, addition, synthetic HIV Gag expression cassettes have been constructed. The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post-entry steps in, viral replication. The expression cassettes of the present invention may be used for the recombinant expression of HIV Gag-polypeptides which may then be used to vaccinate against HIV infection and acquired
                                                                                                                                                                                                                                                                      Expression cassettes encoding the human immunodeficiency virus Gag-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficiency syndrome (AIDS)
                                                                                                                                                                                                                                                                                                                                                        Barnett S, Zur
Greer C, Selby
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                                                                                                                                                                                                                                              Claim 25; Fig 26; 391pp; English.
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                                                                              immunodeficiency syndrome (AIDS).
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                                                      2025 BP;
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Conservative
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M, Walker
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HIV-1; vaccine; anti-HIV; immunogenic; modified; CD4 binding region; V1/V2 loop; bridging sheet; s
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                                                      Modified HIV-1 Env gp160, Val120-Ala204
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Synthetic. WO200039303-A2 Human immunodeficiency virus type 1 isolate SF162

06-JUL-2000.

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30-DEC-1999; 99WO-US31272

31-DEC-1998; 29-SEP-1999; 98US-0114495 99US-0156670

(CHIR ) CHIRON CORP

Barnett Ś Hartog K, Martin m

2000-465745/40.

preparing a vac of HIV subtypes Novel modified HIV Env polypeptides useful as immunizing agents and elicit an immune response against a broad ran

Claim 14; Page 118; 139pp; English

first composition comprising a polynucleotide encoding the Env polypeptide in a priming step and administering a second composition comprising a modified Env polypeptide as a booster in an amount sufficient to induce an immune response in the individual. The first and/or second composition further comprises an adjuvant (claimed). The intracellularly produced Env polypeptides can be used for a number of diagnostic and therapeutic purposes to determine the presence of reactive antibodies/and or Env proteins in a biological sample to aid in the diagnosis of HIV infection or disease status or as measure of response to Novel immunogenic modified human immunodeficiency virus (HIV) envelope (Env) polypeptides having an amino acid deleted or replaced in the region corresponding to residues 420-436 or 119-123 and 199-210 relative to isolate HXB-2 are disclosed. The modified Env polypeptide is based on HIV strain SF162, with numbering relative to isolate HXB-2. The Env polypeptides are modified so as to expose at least part of the CD4 binding region. The modified HIV Env polypeptides, coding polynucleotides and constructs, further comprising an adjuvant, are used for inducing an immune response in an individual. The method involves administering a firm of the code o

Sequence 2310 BP; 477 A; 805 Ç 707 G; 321 T; 0 other;

Query Match Best Local

Similarity

2.9%;

DB 21; Length

Matches 422; 496 762 GTCAAGTCCTACCTAGCGGAAAAGAAAGGACGTCGCGCCAAAGGACATGGTCATGGTGTCC GCCCACTGCAACATCAGCGGCGAGAAGTGGAACAACACCCTGAAGCAGATCGTGACCAAG CCGGACCTGATCCCCTACGTGAGCAGCTGCAAGAGCCCCCAGATGATGCTGGCGGCCATG CCGCTGCCCATGTTCACCAGCTGCTGCCCCGGCTGGATCGCTATGCTGGAGAAATCTTAC CTGAAGGAGAGCGTGGAGATCAACTGCACCCGCCCCAACAACAACACCCCGCAAGAGCATC GGCAGCGAGCTGCTGCACCGCCTCACCGAGCACCTGGAGGCCCACCCGCACTCCGACGAG GAGGGCGTGGTGATCCGCAGCGAGAACTTCACCGACAACGCCAAGACCATCATCGTGCAG CTCGGCTTTGACGAGGTGTTTGACACGCTGTTTGGCGCCCGACCTGACCATCATGGAGGAG ACCCACGGCATCCGCCCCGTGGTGAGCACCCAGCTGCTGCTGAACGGCAGCCTGGCCGAG ACCCTGGGCCTGGCGCGGGGGCCACCACCCCAAGCAGCTGGCCGAGGGCCTCCGCCGC ACCATCGGCCCGGGCGCCTTCTACGCCACCGGCGACATCATCGGCGACATCCGCCAG Conservative 0; Score 69.8; DI Pred. No. 0.00: 0; Mismatches J.0015; 522; Indels 9 675 521 821 761 735 641 615 581 555 795

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1393 AACCTGCTGCGCGCCATCGAGGCCCAGCAGCACCTGCTGCAGCTGACCGTGTG 1445
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Search completed: June 8, 2003, 10:17:54 Job time: 857 secs

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Maximum Match 100%
Listing first 45 s
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 60.4
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-08-403-852D-1
US-08-510-6468-1
US-08-510-6468-1
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US-08-804-439A-13
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4 US-09-103-840A-1
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Sequence 2, Appli
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Patent No. 5215881
Sequence 9, Arrives
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13, Appl
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#### ALIGNMENTS

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RESULT 1
US-08-804-227C-7
                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCI(DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
FILING DATE: February 21, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-8231
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Applic Patent No. 5876991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION
                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 44377 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: DeHoff, Bradley S.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
                                     FEATURE:
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NAME/KEY:
LOCATION:
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CTTY: INDIANAPOLIS
                                                         LOCATION:
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FEATURE:

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US-08-804-227C-7
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Best Local Similarity 43.5%;
Matches 502; Conservative
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CCGGCGAGGCCAAGTACGACTTTGTGGAGATCATGGCCTGCCCCGC---GGGCTGTGTGG
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                                                   CCCTGCGCACCATCAGCCAGGCCCGGCACACCGGAAAGCTCGTCCTGACCATGCCGCCCG
                                                                                                               CCTGGCACCCGTACGGCACGGTCCTGGTCACCGGTGGCACCGGCGCCCTCGGCAGCCGCA 2995
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                                                                              TGCGCGTGGCCGTGGCCAACGGGCTGGGCAACGCCAAGAAGCTGATCACCAAGATGCAGG 1368
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Pred. No. 0.00012;
0; Mismatches 641;
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                       TELEPHONE: 317-276-3885
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36.4
REFERENCE/DOCKET NUMBER:
                                                                   FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: Macintosh 7.0
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,15
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ROSTECK, Paul R., Jr
TITLE OF INVENTION: PLATENOLIDE
NUMBER OF SEQUENCES: 6
                                   LOCATION: FEATURE:
                                                                                                                                                                                             MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: I
NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                   LENGTH: 44377 base pairs
TYPE: nucleic acid
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Kuhstoss, Stuart A.
Rao, Nagaraja R.
Richardson, Mark A.
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LILLY CORPORATE CENTER
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Best Local Similarity 43.5%;
Matches 502; Conservative
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   GCGGCGGCCGCCCGCTCCACCGACAAGGCCATCACGCAGAAGCCGGCAGGCGGCGC 1485
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Pred. No. 0.00012;
0; Mismatches 641;
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Sequence 1, Application US/09428517

Sequence 1, Application US/09428517

Patent No. 6251636

GENERAL INFORMATION:
APPLICANT: Betlach, Mary C.
APPLICANT: Shah, Sanjay Krishnakant
APPLICANT: Tang, Li
APPLICANT: Tang, Li
APPLICANT: Tang, Li
APPLICANT: Tang, Li
CURENT APPLICATION NUMBER: US/09/428,517

CURRENT APPLICATION NUMBER: US/09/428,517

CURRENT FILING DATE: 1999-10-28

EARLIER APPLICATION NUMBER: 60/120,254

EARLIER PILING DATE: 1998-10-29

NUMBER OF SEQ ID NOS: 12

SOCTWARE: Patentin Ver. 2.1

SEQ ID NO 1

LENGTH: 50937
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US-09-428-517-1/c
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US-09-428-517-1
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 376; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                             2.7%; Score 64.6; DB 4; ilarity 45.6%; Pred. No. 0.00018; Conservative 0; Mismatches 419;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kwamena A Aidoo
APPLICANT: Ashish S. Paradkar
TITLE OF INVENTION: DNA Sequence Encor
Patent No. 6232106
TITLE OF INVENTION: Acid Biosynthesis
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
             TELEFAX: (202) 39305350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 0:
FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                     NAME: D. DOUGIAS Price
REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: The vent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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1182 base pairs
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Buliding, 400 Seventh Street, N.W.
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MOLECULE TYPE: DNA (ger
US-09-385-028-19
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   GCCATGGCGATCGGCAAGTGCTCGGACGACGACCGACATCGACCAGGAGCGGGTGACGATC
                                                                                                          GCCGAGGCCGCCGCACGGCACCCCCGGGCCGCTGGCCTGGGACGGCGGCGCGGGCTTC
                                                                                                                                                                                                                     GCGGCGCTGGCCCTGGTCAAGGACATCGCGAGCGACGGCGAGGGCGAGGCCAAGCTGATC
                                                                         GTCAACTCCCCGTTGGTGAAGACCGCCGTGCACGGCTGCGACCCCAACTGGGGCCGGGTC
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43.5%;
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QY 465 CTGGGCCTGGCGCCGGCCCACCCACCCCAAGCAGCTGGCCGAGGGGCCTCCGCCCCCCC 524	Query Match 2.6%; Score 63.4; DB 4; Length 11604; Best Local Similarity 43.5%; Pred. No. 0.0022; Matches 475; Conservative 0; Mismatches 586; Indels 30; Gaps 3;  Qy 405 ACGCGCAAGCACGTCTGCGTGCACGTGGCCTCTCGTGTTGTTGCTGATTTGCCGAGACC 464	; INFORMATION FOR SEQ ID NO: 13: ; SEQUENCE CHARACTERISTICS: ; LENGTH: 11604 base pairs ; TYPE: nucleic acid ; STRANDENNESS: single ; TOPOLOGY: linear ; MOLECULE TYPE: DNA (genomic) US-09-385-028-13	; ATTORNEY/AGENT INFORMATION: ; NAME: D. Douglas Price ; REGISTRATION NUMBER: 24,514 ; REFERENCE/DOCKET NUMBER: 1418/P57452US2 ; TELECOMMUNICATION INFORMATION: ; TELEPAN: (202 638-6666 ; TELEFAX: (202) 3395350 ; TELEFAX: RCA 248593 IDEA UR	APPLICATION NUMBER: US/09/385,028 FILING DATE: CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/790,462 FILING DATE: 29-JAN-1997	COMPUTER READABLE FORM:  COMPUTER READABLE FORM:  COMPUTER: IBM PC compatible  COMPUTER: IBM PC compatible  COPERATING SYSTEM: PC-DOS/MS-DOS  SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)	NUMBER OF EQUENCES: 25  NUMBER OF SEQUENCES: 25  CORRESPONDENCE ADDRESS:  ADDRESSEB: JACOBSON, PRICE, HOLMAN & STERN, PPLC  STREET: The Jenifer Building, 400 Seventh Street, N.W.  CITY: Washington  STAYE: D.C.  COUNTRY: U.S.A.	on US/C	Qy 1458 GCCATCACGCA 1468               Db 1099 GCCATCGCGA 1109  RESULT 5 RESULT 5	Qy 1338 AACGCCAAGAAGCTGATCACCAAGATGCAGGCCGAGGCCAAGTACGACTTTTGTGGAG 1397
RESULT 6 US-09-385-028-1 ; Sequence 1, Application US/09385028	Oy 1398 ATCATGGCCTGCCCGCGGGGCTGTGTGGGCGGCGGCGAGCAGCCCGCCC	OY 1278 ACCAGGAGGACGGCAGGGCGGCCATCACACTGCGCGTGGCCCAACGGCTGGGC 1337	QY 1158 ATGGTGCCCGGGCCCGGGTCCAAGTTTGAGGAGCTGCTGAAGCACCGCGCGCG	Db 6541 TTCGCCAACGGCCTGGCGGGGGGGGGGGGGGGGGGGGGG	Qy 999 GGCGTGGGCTCGGGCGCCGTGTTCGGCACCACCGGCGGTGTCATGGAGGCGGCG·1058	Qy 879 GCCGACCCCACCCTGCGCCAGCTGGACCACCGTCATCACCACCGTGGACCTGGGCCAACATC 938	Oy  765 AAGTCCTACCTAGGGGAAAAGAAAGGAATGGACAAGGAAGGAATGGTCATGGTG 818  Qy  765 AAGTCCTACCTAGCGGAAAAGGAAGGACATGGTCATGGTG 818	645 CTGCCCATGTTCACCAGCTGCTGCCCCGGCTGGATCGCTATGCTGGAGAAAATCTTACCCG	Qy 525 GGCTTTGACGAGGTGTTTGACACGCTGTTTGGCGCCGACCTGACCATCATGGAGGAGGGC 584

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APPLICANT: Kwamena A Aidoo APPLICANT: Ashish S. Paradkar TITLE OF INVENTION: DNA Sequence; Patent No. 6332106
TITLE OF INVENTION: Acid Biosyntic Number Of Serving Patent No. 6332106
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; MOLECULE TYPE: D
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Stre
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Best Local
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TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 1:
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APPLICATION NUMBER: US 08
FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: D. Douglas Price
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REGISTION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202 638-6666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: JACOBSON,
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CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 15079 base pairs
TYPE: nucleic acid
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Pred. No. 0.00024;
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APPLICANT: Rudolf Jung
APPLICANT: Francois Barrieu
APPLICANT: Francois Barrieu
TITLE OF INVENTION: Maize Aquaporins and Uses The
FILE REFERENCE: 0919
CURRENT APPLICATION NUMBER: US/09/372,422A
CURRENT FILING DATE: 1999-08-11
PRIOR PELICATION NUMBER: US 60/098,692
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 49
                                                                                                                                                                                                                                                   Sequence 11, Application US/09372422A Patent No. 6313375 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8216 ATCGCCTCCACCGGGGTGATCGGCCGGCAGTACCCGATGGAGAGCATCCGGGAGCACCTC
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GENERAL INFORMATION:
APPLICANT: Jayne, Susan
APPLICANT: Barbour, Eric
APPLICANT: Meyer, Terry
TITLE OF INVENTION: METHODS FOR THE REFERENCE: moPAT_moCAH
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US-09-003-287-7
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US-09-003-287-7
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CURRENT FILING DATE: 1998-01-06
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 7
LENGTH: 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/09003287 Patent No. 6096947
                                                                                                                                                                           Matches 305;
                                                                                                                                                                                             Query Match
Best Local :
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                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Myrothecium
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LOCATION: (110)...(974)
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                                                                                                                                                                                           Local Similarity
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                                                                                                                                 GGACGCCGACCCCACCCTGCGCCCAGCTGGACCACCATCACCACCGTGGAGCTGGGGCAA
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AATGGGCGTGGGCTCGGGCGCGCGGCGTGTTCGGCACCACCGGCGGTGTCATGGAGGC 1054
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                                                                                                              GGCCATCGTGGACTCCCTCGGCAAGCTCGGCGACGTCAGCTCCTACTCCGTGGAGGACAT
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Pred. No. 0.00024;
0; Mismatches 357;
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Pred. No. 0.00019;
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RESULT 9
US-07-945-283-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                TELEFAX: 309-68
INFORMATION FOR SEQ
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APPLICATION NUMBER: US/07/945,283
FILING DATE: 19920911
CLASSIFICATION: 424
ATTORNEY / ACTIVE
                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Ribando, Curtis P
REGISTRATION NUMBER: 27976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 309-685-4011 ext.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0
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ADDRESSEE: Curtis P.
STREET: 1815 No. 535
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 10
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Pred. No. 0.00044;
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US-08-403-852D-1
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Patent No. 589169
                                                                                                                                 TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                           FILING DATE: 10-MAY-15
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PRICE DATE: 25-SEP-15
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PRIOR CACTION NUMBER: PRICE DATE: 25-SEP-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Biosynthesis Of Streptogramins,
TITLE OF INVENTION: Coding For These Polypeptides AI
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                      FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/403,85
                                                                                                                                                                                                     NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03
TELECOMMUNICATION INFORMATION:
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ORIGINAL SOURCE:
                            MOLECULE TYPE:
HYPOTHETICAL:
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                    TOPOLOGY:
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STRANDEDNESS:
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And Their Use
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US-08-403-852D-1
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43.3%;
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Pred. No. 0.00048;
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RESULT 11
US-08-510-646B-1
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                                                                                                                                                                                                                                           FILING DATE: 03-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR
APPLICATION NUMBER: PCT/FR
FILING DATE: 25-SEP-1993
PRIOR APPLICATION NATA:
APPLICATION NUMBER: FR 92/
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                       TELEFAX: (202) 408-4400 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                       NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
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              TOPOLOGY: 1
MOLECULE TYPE:
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HYPOTHETICAL:
                                                STRANDEDNESS: double
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Blanche, Francis
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ORGANISM: S.P
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                                                                   CACCGGCTCAAGGCCGGCCGGTCTCTGAGCCGGCCGGACCTGTGAGGAGACCTGACGT
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Pred. No. 0.00048;
0; Mismatches 636;
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RESULT 12
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                                                                                                           TELEFAX: (202) 408-4400 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: ETITLE OF INVENTION: ETITLE OF INVENTION: COMMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231,81
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ADDRESSEE: Finnegan, Henderson, Farabow,
STREET: 1300 I Street, N.W., Suite 700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                         REFERENCE/DOCKET NUMBER: 0.
TELECOMMUNICATION INFORMATION
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                    FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                FILING DATE:
PRIOR APPLICATION DATA:
                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                     APPLICATION NUMBER: FR 9: FILING DATE: 25-SEP-1992 ATTORNEY/AGENT INFORMATION:
HYPOTHETICAL:
             TOPOLOGY: 1:
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ZIP: 200
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/403,852 FILING DATE: 10-MAY-1995 APPLICATION NUMBER: PCT/FR 93/00923
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                                                                                                                                                                                         REGISTRATION NUMBER:
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                                                                                                                                       TELEPHONE:
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Thibaut, Denis
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Crouzet, Joel
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Pred. No. 0.00048;
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                                                                                                                                                                Matches
                                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2713 base pairs
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APPLICANT: Bosch, Marnix L.
APPLICANT: Strand, Kurt
TITLS OF INVENTION: GLYCOPROTEIN B OF THE RFHV/KSHV
TITLE OF INVENTION: SUBFAMILY OF HERPES VIRUSES
NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: Haile, Lisa A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                           TELEX:
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ZIP: 92037
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Pred. No.
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                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Vei
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/720,229
FILING DATE: 26-SEP-1996
CLASSIFICATION: 424
CLASSIFICATION: 424
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APPLICANT: Rose, Timothy M.

APPLICANT: Bosch, Marnix L.

APPLICANT: Strand, Kurt

TITLE OF INVENTION: GLYCOPROTEIN B OF THE RFHV/KSHV

TITLE OF INVENTION: SUBFAMILY OF HERPES VIRUSES

NUMBER OF SEQUENCES: 100

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster
ATTORNEY/AGENT INFORMATION:
NAME: SChlift, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 29
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                         CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                       ZIP: 94304-1018
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US-09-103-840A-2/c
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
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INFORMATION FOR SEQ ID NO: 13
SEQUENCE CHARACTERISTICS:
LENGTH: 2713 base pairs
TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: linear
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Pred. No. 0.00049;
0; Mismatches 380
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GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
APPLICANT: VENTER, JOHN C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN

ANALYSIS IN MYCOBACTERIUM

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TYPE: DNA.
TYPE: DNA.
CRGANISM: Mycobacterium tuberculosis
FEATURE:
PEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
SEGID NO 2
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Search completed: June
Job time : 2876 secs
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Best Local Similarity 48.8%;
Matches 163; Conservative
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Perfect score:
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/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3

LENGTH: 2310

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Vall20-Ala204
US-09-476-242-3
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APPLICANT: BARNETT, SUSAN
APPLICANT: HARTOG, KAR'IN
APPLICANT: HARTOG, KAR'IN
APPLICANT: MARTIN, Eric
TITLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES
FILE REFERENCE: 1605.002
CURRENT APPLICATION NUMBER: US/09/476,242
CURRENT FILING DATE: 1999-12-30
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Best Local (
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676 ACCATCGGCCCCGGCCGCCTTCTACGCCACCGGCGACATCATCGGCGACATCCGCCAG
                                           642 CCGCTGCCCATGTTCACCAGCTGCTGCCCCGGCTGGATCGCTATGCTGGAGAAATCTTAC
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Pred. No. 4e-09;
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RESULT 2
US-09-476-242-4
US-09-476-242-4
Sequence 4, Application US/09476242
Patent No. US/0020146683A1
GENERAL INFORMATION:
APPLICANT: BARNETT, Susan
APPLICANT: HARTOG, Karin
APPLICANT: MARTON, Eric
TITLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES
FILE REFERENCE: 1605.002
CURRENT APPLICATION NUMBER: US/09/476,242
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
LENGTH: 2316
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence
US-09-476-242-4
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                                        ACCAAGATGCAGGCCGGCGAGGCCAAGTACGACTTTGTGGAGATCATGGCCTG 1408
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RESULT 3
US-09-476-242-8
; Sequence 8, Application US/09476242
; Patent No. US20020146683A1
; GENERAL INFORMATION:
; APPLICANT: BARNETT, Susan

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APPLICANT: HARTOG, Karin
APPLICANT: MARTIN, Eric
TITLE OF INVENTION: MODIFIED HIV ENV POLYPEP
FILE REFERENCE: 1605.002
CURRENT APPLICATION NUMBER: US/09/476,242
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 8
LENGTH: 2316
TYPE: DNA
ORGANISM: Artificial Sequence
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Pred. No. 4e-09;
0; Mismatches 522;
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GENERAL INFORMATION:
APPLICANT: BARNETT, SUSAN
APPLICANT: BARNETT, SUSAN
APPLICANT: HARTOG, KATIN
APPLICANT: MARTOG, KATIN
APPLICANT: MARTOG, Eric
TITLE OF INVENTION: MODIFIED HIV ENV POLYPEP
FILE REPERENCE: 1005.002
CURRENT APPLICATION NUMBER: US/09/476,242
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 5
LENGTH: 2322
TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 44.3%;
Matches 422; Conservative
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CTGCCCTGCCGCATCAAGCAGATCATCAACCGCTGGCAGGAGGTGGGCCAAGGCCATGTAC
                                    AAGGAGCGCGCATCAACCTGGCCGAGCTGCCCGAGGGGCGAGTGGGACAATCCAATGGGC
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0; Mismatches 522;
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APPLICANT: HARTOG, KAR'IN
APPLICANT: HARTOG, KAR'IN
APPLICANT: MARTIN, Eric
TITLE OF INVENTION: MODIFIED HIV ENV POLYPEP
FILE REFERENCE: 1605.002
CURRENT APPLICATION NUMBER: US/09/476,242
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PALENTIN Ver. 2.0
SEQ ID NO 6
LENGTH: 2328
TYPE: DNA
ORGANISM: Artificial Sequence
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US-09-476-242-6
; Sequence 6, Application US/09476242
; Patent No. US20020146683A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Lys121-Val200
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APPLICANT: HARTOG, Karin
APPLICANT: HARTOG, Karin
APPLICANT: MARTIN, Eric
TITLE OF INVENTION: MODIFIED HIV ENV POLYPEP
FILE REFERENCE: 1605.002
CURRENT APPLICATION NUMBER: US/09/476,242
CURRENT FILING DATE: 199-12-30
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 7
LENGTH: 2334
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
FEATURE:
                                                                          ; OTHER INFORMATION: US-09-476-242-7
Query Match
Best Local Similarity
Matches 422; Conserv
 2.9%;
ilarity 44.3%;
Conservative
                                                                                              Description
   Score 69.8; DB 10;
Pred. No. 4e-09;
0; Mismatches 522;
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US-09-476-242-7; Sequence 7, Application US/09476242; Patent No. US20020146683A1

GENERAL INFORMATION:

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RESULT 7
US-09-476-242-25
Sequence 25, Application US/09476242
Patent No. US20020146683A1
GENERAL INFORMATION:
APPLICANT: BARNETT, Susan
APPLICANT: HARTOG, Karin
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LENGTH: 2358
TYPE: DNA
ORGANISM: Artificial S
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Best Local Similarity 44.3%;
Matches 422; Conservative
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CURRENT APPLICATION NUMBER: US/09/476,
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
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Pred. No. 4e-09;
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CURRENT APPLICATION NUMBER: US/09/808,880
CURRENT FILLING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: US/09/428,517
PRIOR APPLICATION NUMBER: US/09/428,517
PRIOR PRILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/120,254
PRIOR FILLING DATE: 1999-02-16
PRIOR FILLING DATE: 1998-10-29
PNUMBER: OF SEO ID NOS: 12
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Best Local Similarity
Matches 376; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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CACCAGCGAGGACGGCAGGGGCGCATCACACTGCGCGTGGCCGTGGCCAA-----
                                                                                                                                              CATGGTGCCCGCGCCCGGGTCCAAGTTTGAGGAGCTGCTGAAGCACCGCGCCGCCGCGC
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                                                                                                                                                                                                                                                         CGTCGAACTCGACGGCCAGGAGCCGTTCGGCCGTCGGCCCTGGGTCTACGGCGACGTCAG
                                                                                                                                                                                                                                                                                                                                                               CGACGACGGCTCGGAGGACGGGGACCGCACGTCGCTGTCCCTGCCCGGGCCGCCAGGACGA
                                                                                                            GATCGACCGGG----CCGTGTCGATCGCGCGGACGGCGACGGACCGCGGTCGTCTTCGCGTA 3418
                                                                                                                                                                                  GGCGAAGTCGCCCATGACCTTCGAGCTGACGTGGGTCACTCCGCAGGCCGCCCAGGAGGC
                                                                                                                                                                                                                                                                                           CGGCGGTGTCATGGAGGCGGCGCTGCGCACGGCCTATGAGCTGTTCACGGGCACGCCGCT 1096
                                                                      CGCCGAGGCCGCCGCACGGCACCCCCCGGGCCGCTGGCCTGGGACGGCGGCGCGGCTTT
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nilarity 45.6%;
Conservative
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Pred. No. 2.5e-07;
0; Mismatches 419;
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                                                                                                                                                                                                           ; LENGTH: 15952
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-171-311-51
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US-10-171-311-51
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CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US 60/298,159
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR APPLICATION NUMBER: US 60/335,936
PRIOR APPLICATION NUMBER: US 60/335,936
PRIOR FILING DATE: 2001-11-14
NUMBER OF SEO ID NOS: 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 51, Application US/10171311 Publication No. US20030087270A1
                                                                                                                                                                                                                                                                                   SEQ ID NO 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                         Matches 161;
                                                                                                                                                                           Query Match
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APPLICANT:
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APPLICANT: Chen, Yan
APPLICANT: Zhao, Xumei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hoersh, Sebastian
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KI
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: OF CERVICAL CANCER
FILE REFERENCE: MRI-035
FILE REFERENCE: MRI-035
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                                                                                                  1142 GGAGACCAACATCACCATGGTGCCCGGCGCCCGGGTCCAAGTTTGAGGAGCTGCTGAAGCA 1201
                             h 2.7%;
Similarity 49.8%;
61; Conservative `
                                                                                                                                                                                                                                                                                                  FastSEQ
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GGCCGTGGCCGCGGCGTGGTGGGCCGCGAGATCCAGGAGAAGCTGCTGTCGGCCGAGCG
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Kamatkar, Shubhangi
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                                                                                                                                                                                                                                                                                                      for Windows Version 4.0
                                                                    TCGTCATCGACCCCGTGCGCAACCTGAGGCTGTCGGTGGAGGA
                                                                                                                                       Score 63.8; DB Pred. No. 3e-07; Mismatches 1
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                                                                                                                                                                             Length 15952;
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RESULT 11
US-09-476-242-18
; Sequence 18, Application US,
; Patent No. US20020146683A1
; GENERAL INFORMATION:
; APPLICANT: BARNETT, Susan
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US-09-918-995-200
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Best Local
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CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
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TITLE OF INVENTION: NOVEL NUCLEIC
TITLE OF INVENTION: FROM VARIOUS
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TYPE: DNA
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NAME/KEY: misc_feature
LOCATION: (1)...(447)
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                                                                                                                                                                                                                                                                                TGGGCCACAAGGCGCACGAGCTGCTGCACACCCACTAC 1613
                                                                                                                                                                                                                                                                                                                                              GGCGTCCGGAGTCCAGTGCACGTGCAGGAGCTGTACCAGGAGTGGCTGGAGGGGATCA
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Pred. No. 1.3e-07;
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Best Local Similarity 43.9%;
Matches 417; Conservative
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APPLICANT: MARTIN, ETIC
TITLE OF INVENTION: MODIFIED HIV ENV POLYI
FILE REFERENCE: 1605.002
CURRENT APPLICATION NUMBER: US/09/476,242
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 26
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TYPE: DNA
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Pred. No. 2e-0
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Sequence 10, Application US/09476242
PALENT NO. US20020146683A1.
GENERAL INFORMATION:
APPLICANT: BARRETT, Susan
APPLICANT: HARTOG, Karin
APPLICANT: MARTIN, Eric
TITLE OF INVENTION: MODIFIED HIV ENV POLYPEP
FILE REFERENCE: 1605.002
CURRENT APPLICATION UMBER: US/09/476,242
CURRENT ETLING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PALENTIN Ver. 2.0
LENGTH: 2541
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US-09-4
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oust Local Similarity 43.9%;
Matches 417; Conservation
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AAGGAGCGCGGCATCAACCTGGCCGAGCTGCCCGAGGGGCGAGTGGGACAATCCAATGGGC
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                                                             CAGCTGTTCAACAGCACCTGGAACAACACCATCGGCCCCAACAACACCCAACGGCACCATC
                                                                                                       GACCCCACCCTGCGCCAGCTGGACCACGTCATCACCACCGTGGAGCTGGGCAACATCTTC
                                                                                                                                                CCCGAGATCGTGATGCACAGCTTCAACTGCGGCGAGCGCGAGTTCTTCTACTGCAACAGCACC
                                                                                                                                                                                        ATCATGCCCTGCACGCGCAAGCAGTCGGAGGCTGACCGCGACTGGTTCTGTGTGGACGCC
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                                                                                                                                                                                                                                                                                                                     GCCCACTGCAACATCAGCGGCGAGAAGTGGAACAACACCCTGAAGCAGATCGTGACCAAG
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Pred. No. 2e-07;
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CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 22, Application U
Patent No. US20020146683A1
                                                                                                                                                                                                                                                                                                                                             Matches 426;
                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.6%;
Best Local Similarity 44.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: BARNETT Susan
APPLICANT: HARTOG, Karin
APPLICANT: MARTIN, Eric
TITLE OF INVENTION: MODIFIED HIV
FILE REFERENCE: 1605.002
                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 2298
TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                          CAAGACCATCATCGTGCAGCTGAAGGAGAGCGTGGAGATCAA---CTGCACCCGCCCCAA
                                                                                                                             GGAGGGCAGCGAGCTGCACCGCCTCACCGAGCACCTGGAGGCCCCACCCGCACTCCGA
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        CAACAACACCCGCAAGAGCATCACCATCGGCCCCGGCCGCGCCTTCTACGCCACCGGCGA
                                CGAGCCGCTGCCCATGTTCACCAGCTGCTGCCCGGCTGGATCGCTATGCTGGAGAAATC 697
                                                                                                                                                                                                                                                            CGTGAGCACCGTGCAGTGCACCCACGGCATCCGCCCCGTGGTGAGCACCCAGCTGCTGCT
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                                                                                                                                                                                                                                                                                                                                             Score 62.6; DB 10;
Pred. No. 3.7e-07;
0; Mismatches 519;
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Sequence 23, Application US/09476242
Patent No. US20020146683A1
GENERAL INFORMATION:
APPLICANT: BARNETT, Susan
APPLICANT: MARTIN, Eric
TITLE OF INVENTION, MODIFIED HIV ENV POLYPER
FILE REFERENCE: 1605.002
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
LENGTH: 228
TYPE: DNA
ORGANISM: Artificial Sequence
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US-09-476-
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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Vall20-Ile201B; Ile424-Ala433
-09-476-242-23
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US-09-476-242-24 US-09-476-242-24 ; Sequence 24, Application US/09476242 ; Patent No. US20020146683A1

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GENERAL INFORMATION:
APPLICANT: HARNETT, SUBBIN
APPLICANT: HARTOG, KARÍN
APPLICANT: MARTOG, ERÍC
ITILE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES
FILE REFERENCE: 1605.002
CURRENT APPLICATION NUMBER: US/09/476,242
CURRENT FILING DATE: 199-12-30
RUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 24
LENGTH: 2298
TYPE: DNA
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Vall20-Thr202;
; OTHER INFORMATION: Ile424-Ala433
US-09-476-242-24
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GAACAACCTGCTGCGCGCCATCGAGGCCCAGCAGCACCTGCTGCAGCTGACCGTGTG 1433
                                                               CAGCCTGACCCTGACCGTGCA---GGCCCGCCAGCTGCTGAGCGGCATCGTGCAGCAGCA 1376
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Search completed: June 8, 2003, 14:36:16 Job time: 383 secs

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## ALIGNMENTS

RESULT 1

source	FEATURES							COMMENT	JOURNAL			TITLE		AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	BI717904
1657 /organism="Chlamydomonas reinhardtii"	Location/Qualifiers	Email: chauser@duke.edu.	Fax: 919 613 8177	Tel: 919 613 8159	Durham, NC 27708-1000	Duke University	DCMB Box 91000	Contact: Charles Hauser	Unpublished (2001)	Vascular Plants, Project: 1031	Unicellular System for Analyzing Gene Function and Regulation in	Analyses of the Chlamydomonas reinhardtii Genome: A Model,	,P., McDermott,J.P., Shrager,J., Silflow,C. and Stern,D.	Grossman, A., Chang, CW., Davies, J., Harris, E., Hauser, C., Lefebvre	1 (bases 1 to 657)	Chlamydomonadaceae; Chlamydomonas.	Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;	Chlamydomonas reinhardtii	Chlamydomonas reinhardtii.	EST.	BI717904.1 GI:15693599	BI717904	Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.	1031022F12.y1 C. reinhardtii CC-1690, Stress II (normalized),	BI717904 657 bp mRNA linear EST 19-SEP-2001	

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BASE COUNT
ORIGIN
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/db xref="taxon:3055"
/clone lib="C. reinhardtii CC-1690, Stress II (normalized
), LamEda Zap II"
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Chlamydomonas reinhardtii
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Fax: 919 613 8177
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DCMB Box 91000
Duke University
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TTGCGCGGCTGCCGCACCCGCTGCGGAGGCGCCTTTGAGTCATGTCCAGCAGGCGCTCGC
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                                                             CACCGTGCGTGTAGCCCTTGCAACACTTGAGGCGCCCGCACGCCGCCTAGGCAACGTCGC 316
                                                                                                                                              TATTCGCGGCAGCTCCTGCAGGGCGGGCAGGTCGCCCCCCCGCGCTCCGCTCGCAGCCAG
                                                                                                                    TATTCGCGGCAGCTCCTGCAGGGCGCGCGCAGGTCGCCCCCCGCGCTCCGCTCGCAGCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pBluescript II SK-; Site 1: EcoRI; Site 2: XhoI; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO2 and HS medium bubbled with 5% CO2. PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda synthesized. The cDNA was directionally cloned into lambda SAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."
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/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, :
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C. reinhardtii CC-1690, normalized,
reinhardtii CDNA, mRNA sequence.
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Pred. No. 4.5e-119;
0; Mismatches 7;
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source /organism="CC-1690 wild type mt+ 21gr" /strain="CC-1690 wild type mt+ 21gr" /strain="CC-1690 wild type mt+ 21gr" /clone lib="CC reinhardtii CC-1690, Stress II (normalized), Lambda Zap II" /note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: XhOI; Stress condition II library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (NH4+ - containing) and shifted to TAP - NO3- (24hrs); H2 production conditions (0, 12hr, 24hr) see Mellis et al., (2000) Plant Phys. 12: 127-135; TAP + H2O2 (1, 12, 24 hr); TAP + Sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr); PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda Zap II (Stratagene) in the EcoRI (5') and XhoRI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with Exassist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome	Tel: 919 613 8159 Fax: 919 613 8177 Email: chauser@duke.edu. FEATURES Location/Qualifiers	JOURNAL Unpublished (2001) COMMENT Contact: Charles Hauser DCMB Box 91000 DUKE University Duke University	arris, E., Hause; ow, C. and Stern, cii Genome: A Mc function and Re	3	RESULT 3  BM003317  BM003317  BM003317  DEFINITION 1031109G06.y1 C. reinhardtii CC-1690, Stress II (normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.  ACCESSION BM003317	Qy 617 GGAGGCCCACCCGCACTCCGACGACGACGCTGCCCATGTTCACCAGCTG 664	Qy 557 CGCCGACCTGACCATCATGGAGGAGGGCAGCTGCTGCACCGCCTCACCGAGCACCT 616	Qy 497 GCAGCTGGCCGAGGGCCTCCGCCTCGGCTTTGACGAGGTGTTTGACACGCTGTTTGG 556	Qy 437 GGCCGTTCGTGTCGCTATTGCCGAGACCCTGGGCCTGGCGGCGGCGACCACCACCCCAA 496	Qy 377 CGAGCTTGCCAAGGCCCAAGGACGCCCACGCGCGAAGCACGTCTGCGTGCAGGTGGCTCC 436	Db 301 TTGCGCGCTGCCGCACCGGTGCGGAGGCGCTTTGAGTCATGTCCAGCAGGCGCTCGC 360
RESULT 4 B1716102 B1716102 B1716102 B1716102 B1716103 CC-1690, Stress II (normalized), Lambda Zap II (hlamydomonas reinhardtii cDNA, mRNA sequence.  ACCESSION B1716102 B1716102 VERSION B1716102 Chlamydomonas reinhardtii. Chlamydomonas reinhardtii. Chlamydomonas reinhardtii. Chlamydomonas reinhardtii. Chlamydomonadaceae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.  REFERENCE AUTHORS P. McDermott, J. P. Shrager, J., Harris, E., Hauser, C., Lefebvre, P., McDermott, J. P., Shrager, J., Silflow, C. and Stern, D. Analyses of the Chlamydomonas reinhardtii Genome: A Model, Uncellular System for Analyzing Gene Function and Regulation in Vascular Plants. Project: 1031 COMMENT CCMB Box 91000	QY 1355 CACCAAGATGCAGGCCGGCGAGGCCAAGTACGACTTT 1391	Db 488 CGCACCCCGGCCGGCCGGCCGGACGACGACGACGACGACG	QY         1175         GTCCAAGTTTGAGGAGCTGCTGAAGCACCGCGCGCGCGCG	1115 CGAGGTGCGCGGCATGGACGGCATCAAGGAGACCAACATCACCATGGTGCCCGCGCCCGG	Oy 995 AATGGGCGTGGGCTCGGGCGTGCTGTTCGGCACCGGCGTGTCATGGAGGC 1054	OY 935 CATCTTCAAGGAGCGCGGCATCAACCTGGCCGAGGGCCGAGGGGCGAGTGGGACAATCC 994	OY 875 GGACGCCGACCCCACCCTGCGCCAGCTGGACCACCGTCATCACCACCGTGGAGCTGGGCAA 934	QY 815 GGTGTCCATCATGCCCTGCACGCGCAAGCAGTCGGAGGCTGACCGCGACTGGTTCTGTGT 874	OY 755 GGCCATGGTCAAGTCCTACCTAGCGGAAAAGAAGGGCATCGCGCCAAAGGACATGGTCAT 814	Query Match 26.6%; Score 637; DB 13; Length 644; Best Local Similarity 100.0%; Pred. No. 5.4e-119; Matches 637; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	BASE COUNT 118 a 213 c 230 g 83 t ORIGIN

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Durham, NC 27708-1
Tel: 919 613 8159
Fax: 919 613 8177
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Pred. No. 2.4e-114;
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Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C., Lefebv,P., McDermott,J.P., Shrager,J., Silflow,C. and Stern,D., Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants. Project: 1031
Unpublished (2001)
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EST.
Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophycese; Volvocales;
Chlamydomonadacese; Chlamydomonas.
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Tel: 919 613 8159
Fax: 919 613 8177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Charles Hauser
DCMB Box 91000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: chauser@duke.edu.
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/db_xref="taxon:3055"
/clone_lib="C._reinhardtii CC-1690, Stress II (normalized
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BE724427.1 GI:10125723
EST.
Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre, McDermott,J.P., Silflow,C., Stern,D. and Surzycki,R. Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulati Vascular Plants; project phase 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BE724427 601 bp mRNA linear EST 894076B10.yl C. reinhardtii CC-1690, normalized, Lambda Chlamydomonas reinhardtii cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                             Vascular Plants; project phase
Unpublished (2000)
Contact: Charles Hauser
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                                                                                                                                                                                                     B Box 91000
e University
ham, NC 27708-1000
: 919 613 8159
: 919 613 875
                                                                                                                                                                                          chauser@duke.edu
/noce="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: XhOI; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (acetate-containing) medium in the
                                                                                        /organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, n
                                                                                                                                                                          Location/Qualifiers
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                                                                                        reinhardtii CC-1690, normalized,
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BASE COUNT
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                                  86
                   ambient levels of CO2 and HS medium bubbled with 5% CO2. PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda ZAP II (Stratagene) in the EcoRI (5′) and XhoI (3′) sites. pBluescript II SK-plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."
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Similarity

24.9**%**; 99.5**%**;

12;

Length

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REFERENCE
AUTHORS
TITLE
                                                                                                    ACCESSION
VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                       RESULT 7
AV389547
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                                                      Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Ellaryota, Viridiplantae, Chlorophyta;
Chlamydomonadaceae, Chlamydomonas.
1 (bases 1 to 558)
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            Asamizu,E., Nakamura,Y., Sato,S., Fukuzawa,H. and Tabata,S. A large scale structural analysis of cDNAs in a unicellular alga, Chlamydomonas reinhardtii. I. Generation of 3433
                                                                                                                                                            AV389547
AV389547 Chlamydomonas cDNA clone CM044d10_r, AV389547
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 non-redundant
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reinhardtii C9
mRNA sequence.
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Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp/en/plant/.
                     BG848385
1024021E05.yl (
Chlamydomonas )
BG848385
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/clone="CM044d10 r"
/clone="Ch1emydomonas reinhardtii C9"
/clone_lib="Chlemydomonas reinhardtii C9"
/dev stage="photoautotrophic growth"
/note="Vector: pBluescriptII SK-; Site_1:
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reinhardtii cDNA, mRNA sequence
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Pred. No. 1.1e-102;
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Tel: 919 613 8159
Fax: 919 613 8177
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                             ATACGACAACGGGGCCCGTGAGGATTGAGCACTTGACTCGCGAACTTATGAACGTAGCGC 2219
                                                                               ATGCGCACGTTGTGCGCTGGTGGGCGGGAACGTGGGTAGCATTTAGGCTAGCTGGC
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Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P., McDermott,J.P., Silflow,C., Stern,D. and Surzycki,R. Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation Vascular Plants; project phase 2
Unpublished (2000)
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Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
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DCMB Box 91000
Duke University
GGTTGGAAGCTAAACATGTTTGGGAACAATTCATCTTACTAAAGCGTGTGGGGGTTGAGG
                                                                                                                                                                              TCCAGGGCACGTCGGAATGGCGCGTGCCCCATCAACGCAAATTCTTGGCCTTCATCGCTTC
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                                                                regaratigaaectecacaaacctecatictatitiectietitacacetecccaatctt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chauser@duke.edu
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/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized,
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95.7%;
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	Ouery Match 22.7%; Score 543.8; DB 13; Length 599; Best Local Similarity 99.6%; Pred. No. 4.1e-100; Matches 545; Conservative 0; Mismatches 2; Indels 0; Gaps
BG84834. EST. Chlamydom Chlamydom Eukaryota Ellamydom 1 (bases Grossman, McDermott Unicellul Vascular Unpublish Contact: DCMB Box Duke Univ	o xref="taxon:3055"  Lambda Zap II"  te="Vector: pBluescript II SK-; Site_1  l; Stress condition II library, constricts and Jeffrey McDermott, combines cpl  ls grown to mid-log phase in TAP (NH4+  shifted to TAP - NO3- (24hrs); H2 pro-  ditions (0, 12hr, 24hr) see Melis et a  ps. 12: 127-135; TAP + H202 (1, 12, 24-  thitol (1, 2, 6, 24 hr); TAP + Cd (1, 2,  YA MRNA was purified from each sample,  nthesized. The cDNA was directionally c  pi (Stratagene) in the EcoRI (5') and  es pBluescript II SK- plasmids were exhaba ZAP clones by superinfection with  hod 4 described in Bonaldo et al., (19)  search 6: 791-806."  172 c 207 g 97 t
RESULT 10 BG848384/c BG848384 LOCUS DEFINITION 1024021E05.x2 C. Chlamydomonas re ACCESSION BG848384	Purnam, NC 27708-1000 Tel: 919 613 8159 Fax: 919 613 8177 Email: chauser@duke.edu. FEATURES Location/Qualifiers Source 10.599 /organism="CC-1690 wild type mt+ 21gr"
Db 481 GCGGGTCAAATGT  Qy 1838 AGTAGGC 1844              Db 541 AGTTGCC 547	JOURNAL Unpublished (2001) COMMENT Contact: Charles Hauser DCMB Box 91000 Duke University
361 1718 421 1778	Chlamydomonas reinhardtii.  SM Chlamydomonas reinhardtii.  SM Chlamydomonas reinhardtii.  SE Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocal Chlamydomonadaceae; Chlamydomonas.  1 (bases 1 to 599)  5 (Grossman, A., Chang, CW., Davies, J., Harris, E., Hauser, C., Lef , P., McDermott, J.P., Shrager, J., Silflow, C. and Stern, D. Analyses of the Chlamydomonas reinhardtii Genome: A Model, This of the Chlamydomonas reinhardtii Genome: A Model,
Oy 1538 CATCCGCGAGCTGT	RESULT 9 BI716925 BI716925 LOCUS BI716925 DEFINITION 1031013G11.yl C. reinhardtii CC-1690, Stress II (normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence. ACCESSION BI716925 VERSION BI716925.1 GI:15692620 KEYWORDS EST.
Oy 1358 CAAGATGCAGGCCG	Oy 2220 TTTATACCCACCGTATGACGATTGACGTTAGGCAACCAGGCGGTAGGAAGGCGGAG 2279

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/note="Vector: pBluescript II SK-; Site 1: EcoRI; Site 2: XhoI; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells,grown to
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|n="CC-1690 wild type mt+ 21gr"
|ref="taxon;3055"
|}_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
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on/Qualifiers
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ON AV396217 Chlamydomonas reinhardtii C9 Chlamydomonas recona clone CL58b09_r 5', mRNA sequence.

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Pred. No. 2.7e-99;
D; Mismatches 37;
   Sato, S., Fukuzawa, H. and Tabata, S. analysis of cDNAs in a unicellular
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AV396237 Chlamydomonas reinhardtii C9 Chlamydomonas cDNA clone CL58a12\_r 5', mRNA sequence.

EST 23-APR-2002 reinhardtii

VERSION KEYWORDS

AV396237.1 EST.

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SOURCE

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E 20152988
Contact: Yasukazu Nakamura
The First Laboratory for Plant Ge
Kazusa DNA Research Institute
Yana 1532-3, Kisatazu, Chiba 292
Email: ynakamu@kazusa.or.jp, URL
Location/Qualifiers
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/strain="C9"
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/clone="CL58b09_r"
/clone_lib="Ch18mydomonas reinhardtii
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URL:http://www.kazusa.
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1 (bases 1 to 499)

Asamizu,E., Nakamura,Y., Sato,S., Fukuzawa,H. and Tabata,S. A large scale structural analysis of cDNAs in a unicellular alga, Chlamydomonas reinhardtii. I. Generation of 3433 non-redundant expressed sequence tags

DNA Res. 6 (6), 369-373 (1999)
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AV386674
AV386674 Chlamydomonas reinhardtii C9
CDNA clone CM004all_r, mRNA sequence.
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Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Yana 1532-3, Kisarazusa or jp, URL:http://www.kazusa.or.jp/en/plant/
Location/Qualifiers
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Contact: Yasukazu Nakamura
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/db_xref="taxon:3055"
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/clone="C158a12_r"
/clone_lib="Chlamydomonas reinhardtii
/clone_lib="Chlamydomonas reinhardtii
/dev_stage="photoautotrophic growth"
/note="Vector: pBluescriptII SK-; Site
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Asamizu, E., Nakamura, Y., Sato, S., Fukuzawa, H. and Tabata, S. Asamizu, E., Nakamura, Y., Sato, S., Fukuzawa, H. and Tabata, S. Alsamizu, Chlamydomonas reinhardtii. I. Generation of 3433 non-redundant expressed sequence tags
DNA Res. 6 (6), 369-373 (1999)
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Chlamydomonas reinhardtii
Eukaryota; Viridiplantas; Chlorophyta; Chlorophyceae;
Chlamydomonadaceae; Chlamydomonas.
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Location/Qualifiers
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| Strain="C9" |
| Ab xref="taxon:3055" |
| Clone="CM004a11_r" |
| Clone_11b="Chlamydomonas reinhardtii C9" |
| Cdev_stage="photoautotrophic growth" |
| note="Vector: pBluescriptII SK-; Site_1:
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URL:http://www.kazusa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C., Lefebv,P., McDermott,J.P., Shrager,J., Silflow,C. and Stern,D. Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants. Project: 1031
Unpublished (2001)
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Chlamydomonas reinhardti
Chlamydomonas reinhardt; Chlorophyta; Chlorophyceae; Volvocales;
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                 TCCAGGGCACGTCGGAATGGCGCGTGCCCATCAACGCAAATTCTTGGCCTTCATCGCTTC 1979
                                                                                                                                                                                                                                                                                                                       GGCATTAGGCGTAGGTACTGGCATGAGGGAGCGCGCCTTGCTAACCGAATGGCGTATCCC 1919
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        GGTTGGAAGCTAAACATGTTTGGGAACAATTCATCTTACTAAAGCGTGTGGGGGGTTGAGG
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POlyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda Synthesized from the EcoRI (5') and XhoRI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806."
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/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, Stress II (normalized), Lambda Zap II"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C., Lefeby, P., McDermott, J.P., Shrager, J., Silflow, C. and Stern, D. Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants. Project: 1024b
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BI532214 631 bp mRNA linear EST 29-AU 1024119G12.x1 C. reinhardtii CC-1690, normalized, Lambda Zap Chlamydomonas reinhardtii cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chlamydomonas reinhardtii
Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
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Fax: 919 613 8177
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Durham, NC 27708-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Charles Hauser
DCMB Box 91000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: chauser@duke.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGATGCATTGCAAACGCCTGTAAAAGAACGGCATAG 2315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTATACCCCCGTATGCGATTGACGTTGGTGTAGGCAACCAGGCGGTAGGAAGGCGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 631)
                                                                                                     inote="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: XhoI; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO2 and HS medium bubbbled with 5% CO2. PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda SAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites. pBluescript II SK. plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 631
                  19.8%;
Score 476; DB 13;
Pred. No. 2.3e-86;
0; Mismatches 25;
                                               Length 631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 29-AUG-2001
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Query Match Best Local Similarity Matches 491; Conserv

Conservative

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Gaps

	rch completed: June 8, 2003, 12:43:28
	2280 AGATGCATTGCAAAĆGCCTGTAAAAGAACGGCATAG 2315 
2279 43	2220 TITATACCCACCGTATGCGATTGACGTTGGTGTAGGCAACCAGGCGGTAGGAAGGCGGAG
2219 103	2160 ATÁCGACAACGGGGCCCGTGAGGATTGAGCACTTGACTCGCGAACTTATGAACGTAGCGC
2159 163	2100 ATGCGCACGTTGTGCGCTGGTGGGTGGGCGGAACGTGGGTAGCATTTAGGCTAGCTGGC
2099	2040 GGTTGGAAGCTAAACATGTTTGGGAACAATTCATCTTACTAAAGCGTGTGGGGGTTGAGG
2039 283	1980 TGGATATTGAAGCTGCACAAACCTGCATTCTATTTGCTTGTTTACACGTGCCCCAATCTT
1979 343	1920 TCCAGGGCACGTCGGAATGGCGCGTGCCCATCAACGCAAATTCTTGGCCTTCATCGCTTC
1919 403	1860 GGCATTAGGCGTAGGTACTGGCATGAGGGAGCGCGGCTTGCTAACCGAATGGCGTATCCC
1859 463	1800 TGAGTGGTGTCACAGCATGGGGCACGTGTGCGGAAGGCCAGTAGGCTGTTCACTGCACGCT

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